OIPE

RAW SEQUENCE LISTING DATE: 12/20/2001
PATENT APPLICATION: US/10/007,078 TIME: 14:09:27

Input Set : A:\RTS-0236 Sequence Listing.txt
Output Set: N:\CRF3\12202001\J007078.raw

PS

Does Not Comply
Corrected Diskette Needed

```
      4 <110> APPLICANT: Donna T. Ward
      5       Andrew T. Watt
      7 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF EIF2C1 EXPRESSION
      9 <130> FILE REFERENCE: RTS-0236
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/007,078
C--> 11 <141> CURRENT FILING DATE: 2001-11-08
     11 <160> NUMBER OF SEQ ID NOS: 88
     14 <210> SEQ ID NO: 1
     15 <211> LENGTH: 20
     16 <212> TYPE: DNA
     17 <213> ORGANISM: Artificial Sequence
     19 <220> FEATURE:
     21 <223> OTHER INFORMATION: Antisense Oligonucleotide
     23 <400> SEQUENCE: 1
     24 tccgtcatcg ctcctcaggg                                              20
     27 <210> SEQ ID NO: 2
     28 <211> LENGTH: 20
     29 <212> TYPE: DNA
     30 <213> ORGANISM: Artificial Sequence
     32 <220> FEATURE:
     34 <223> OTHER INFORMATION: Antisense Oligonucleotide
     36 <400> SEQUENCE: 2
     37 atgcattctg cccccaagga                                              20
     40 <210> SEQ ID NO: 3
     41 <211> LENGTH: 7478
     42 <212> TYPE: DNA
     43 <213> ORGANISM: Homo sapiens
     45 <220> FEATURE:
     47 <220> FEATURE:
     48 <221> NAME/KEY: CDS
     49 <222> LOCATION: (214)...(2787)
     51 <400> SEQUENCE: 3
     52 actggcagct ggccgggcgc tcgcagtggg agctgctgca ggctccgcgg cggcggcaac    60
     53 ggaggctgcg ggggcggcgg cgcgagcggc cgggcttggt aggggagccg agcccggccc   120
     54 gggatcccga gcagcgagag tgtggggtac ctaggcccct cacgctggac ttcacagtct   180
     55 ccgggccgcc tgacctccgc acgggtatat ggg atg gaa gcg gga ccc tcg gga    234
     56                                     Met Glu Ala Gly Pro Ser Gly
     57                                       1               5
     59 gca gct gcg ggc gct tac ctg ccc ccc ctg cag cag gtg ttc cag gca     282
     60 Ala Ala Ala Gly Ala Tyr Leu Pro Pro Leu Gln Gln Val Phe Gln Ala
     61          10                  15                  20
     63 cct cgc cgg cct ggc att ggc act gtg ggg aaa cca atc aag ctc ctg     330
     64 Pro Arg Arg Pro Gly Ile Gly Thr Val Gly Lys Pro Ile Lys Leu Leu
     65      25                  30                  35
     67 gcc aat tac ttt gag gtg gac atc cct aag atc gac gtg tac cac tac     378
     68 Ala Asn Tyr Phe Glu Val Asp Ile Pro Lys Ile Asp Val Tyr His Tyr
     69  40                  45                  50                  55
```

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```
71 gag gtg gac atc aag ccg gat aag tgt ccc cgt aga gtc aac cgg gaa     426
72 Glu Val Asp Ile Lys Pro Asp Lys Cys Pro Arg Arg Val Asn Arg Glu
73                  60                  65                  70
75 gtg gtg gaa tac atg gtc cag cat ttc aag cct cag atc ttt ggt gat     474
76 Val Val Glu Tyr Met Val Gln His Phe Lys Pro Gln Ile Phe Gly Asp
77              75                  80                  85
79 cgc aag cct gtg tat gat gga aag aag aac att tac act gtc aca gca     522
80 Arg Lys Pro Val Tyr Asp Gly Lys Lys Asn Ile Tyr Thr Val Thr Ala
81          90                  95                  100
83 ctg ccc att ggc aac gaa cgg gtc gac ttt gag gtg aca atc cct ggg     570
84 Leu Pro Ile Gly Asn Glu Arg Val Asp Phe Glu Val Thr Ile Pro Gly
85      105                 110                 115
87 gaa ggg aag gat cga atc ttt aag gtc tcc atc aag tgg cta gcc att     618
88 Glu Gly Lys Asp Arg Ile Phe Lys Val Ser Ile Lys Trp Leu Ala Ile
89 120                 125                 130                 135
91 gtg agc tgg cga atg ctg cat gag gcc ctg gtc agc ggc cag atc cct     666
92 Val Ser Trp Arg Met Leu His Glu Ala Leu Val Ser Gly Gln Ile Pro
93                  140                 145                 150
95 gtt ccc ttg gag tct gtg caa gcc ctg gat gtg gcc atg agg cac ctg     714
96 Val Pro Leu Glu Ser Val Gln Ala Leu Asp Val Ala Met Arg His Leu
97              155                 160                 165
99 gca tcc atg agg tac acc cct gtg ggc cgc tcc ttc ttc tca ccg cct     762
100 Ala Ser Met Arg Tyr Thr Pro Val Gly Arg Ser Phe Phe Ser Pro Pro
101         170                 175                 180
103 gag ggc tac tac cac ccg ctg ggg ggt ggg cgc gaa gtc tgg ttc ggc     810
104 Glu Gly Tyr Tyr His Pro Leu Gly Gly Gly Arg Glu Val Trp Phe Gly
105     185                 190                 195
107 ttt cac cag tct gtg cgc cct gcc atg tgg aag atg atg ctc aac att     858
108 Phe His Gln Ser Val Arg Pro Ala Met Trp Lys Met Met Leu Asn Ile
109 200                 205                 210                 215
111 gat gtc tca gcc act gcc ttt tat aag gca cag cca gtg att gag ttc     906
112 Asp Val Ser Ala Thr Ala Phe Tyr Lys Ala Gln Pro Val Ile Glu Phe
113                 220                 225                 230
115 atg tgt gag gtg ctg gac atc agg aac ata gat gag cag ccc aag ccc     954
116 Met Cys Glu Val Leu Asp Ile Arg Asn Ile Asp Glu Gln Pro Lys Pro
117             235                 240                 245
119 ctc acg gac tct cag cgc gtt cgc ttc acc aag gag atc aag ggc ctg    1002
120 Leu Thr Asp Ser Gln Arg Val Arg Phe Thr Lys Glu Ile Lys Gly Leu
121         250                 255                 260
123 aag gtg gaa gtc acc cac tgt gga cag atg aag agg aag tac cgc gtg    1050
124 Lys Val Glu Val Thr His Cys Gly Gln Met Lys Arg Lys Tyr Arg Val
125     265                 270                 275
127 tgt aat gtt acc cgt cgc cct gct agc cat cag aca ttc ccc tta cag    1098
128 Cys Asn Val Thr Arg Arg Pro Ala Ser His Gln Thr Phe Pro Leu Gln
129 280                 285                 290                 295
131 ctg gag agt gga cag act gtg gag tgc aca gtg gca cag tat ttc aag    1146
132 Leu Glu Ser Gly Gln Thr Val Glu Cys Thr Val Ala Gln Tyr Phe Lys
133                 300                 305                 310
135 cag aaa tat aac ctt cag ctc aag tat ccc cat ctg ccc tgc cta caa    1194
```

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```
136 Gln Lys Tyr Asn Leu Gln Leu Lys Tyr Pro His Leu Pro Cys Leu Gln
137             315                 320                 325
139 gtt ggc cag gaa caa aag cat acc tac ctt ccc cta gag gtc tgt aac    1242
140 Val Gly Gln Glu Gln Lys His Thr Tyr Leu Pro Leu Glu Val Cys Asn
141         330                 335                 340
143 att gtg gct ggg cag cgc tgt att aag aag ctg acc gac aac cag acc    1290
144 Ile Val Ala Gly Gln Arg Cys Ile Lys Lys Leu Thr Asp Asn Gln Thr
145     345                 350                 355
147 tcg acc atg ata aag gcc aca gct aga tcc gct cca gac aga cag gag    1338
148 Ser Thr Met Ile Lys Ala Thr Ala Arg Ser Ala Pro Asp Arg Gln Glu
149 360                 365                 370                 375
151 gag atc agt cgc ctg atg aag aat gcc agc tac aac tta gat ccc tac    1386
152 Glu Ile Ser Arg Leu Met Lys Asn Ala Ser Tyr Asn Leu Asp Pro Tyr
153                 380                 385                 390
155 atc cag gaa ttt ggg atc aaa gtg aag gat gac atg acg gag gtg aca    1434
156 Ile Gln Glu Phe Gly Ile Lys Val Lys Asp Asp Met Thr Glu Val Thr
157             395                 400                 405
159 ggg cga gtg ctg ccg gcg ccc atc ttg cag tac ggc ggc cgg aac cgg    1482
160 Gly Arg Val Leu Pro Ala Pro Ile Leu Gln Tyr Gly Gly Arg Asn Arg
161         410                 415                 420
163 gcc att gcc aca ccc aat cag ggt gtc tgg gac atg cgg ggg aaa cag    1530
164 Ala Ile Ala Thr Pro Asn Gln Gly Val Trp Asp Met Arg Gly Lys Gln
165     425                 430                 435
167 ttc tac aat ggg att gag atc aaa gtc tgg gcc atc gcc tgc ttc gca    1578
168 Phe Tyr Asn Gly Ile Glu Ile Lys Val Trp Ala Ile Ala Cys Phe Ala
169 440                 445                 450                 455
171 ccc caa aaa cag tgt cga gaa gag gtg ctc aag aac ttc aca gac cag    1626
172 Pro Gln Lys Gln Cys Arg Glu Glu Val Leu Lys Asn Phe Thr Asp Gln
173                 460                 465                 470
175 ctg cgg aag att tcc aag gat gcg ggg atg cct atc cag ggt caa cct    1674
176 Leu Arg Lys Ile Ser Lys Asp Ala Gly Met Pro Ile Gln Gly Gln Pro
177             475                 480                 485
179 tgt ttc tgc aaa tat gca cag ggg gca gac agc gtg gag cct atg ttc    1722
180 Cys Phe Cys Lys Tyr Ala Gln Gly Ala Asp Ser Val Glu Pro Met Phe
181         490                 495                 500
183 cgg cat ctc aag aac acc tac tca ggg ctg cag ctc att att gtc atc    1770
184 Arg His Leu Lys Asn Thr Tyr Ser Gly Leu Gln Leu Ile Ile Val Ile
185     505                 510                 515
187 ctg cca ggg aag acg ccg gtg tat gct gag gtg aaa cgt gtc gga gat    1818
188 Leu Pro Gly Lys Thr Pro Val Tyr Ala Glu Val Lys Arg Val Gly Asp
189 520                 525                 530                 535
191 aca ctc ttg gga atg gct acg cag tgt gtg cag gtg aag aac gtg gtc    1866
192 Thr Leu Leu Gly Met Ala Thr Gln Cys Val Gln Val Lys Asn Val Val
193             540                 545                 550
195 aag acc tca cct cag act ctg tcc aac ctc tgc ctc aag atc aat gtc    1914
196 Lys Thr Ser Pro Gln Thr Leu Ser Asn Leu Cys Leu Lys Ile Asn Val
197             555                 560                 565
199 aaa ctt ggt ggc att aac aac atc cta gtc cca cac cag cgc tct gcc    1962
200 Lys Leu Gly Gly Ile Asn Asn Ile Leu Val Pro His Gln Arg Ser Ala
```

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Input Set : A:\RTS-0236 Sequence Listing.txt
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```
201          570                 575                 580
203 gtt ttt caa cag cca gtg ata ttc ctg gga gca gat gtt aca cac ccc    2010
204 Val Phe Gln Gln Pro Val Ile Phe Leu Gly Ala Asp Val Thr His Pro
205     585                 590                 595
207 cca gca ggg gat ggg aaa aaa cct tct atc aca gca gtg gta ggc agt    2058
208 Pro Ala Gly Asp Gly Lys Lys Pro Ser Ile Thr Ala Val Val Gly Ser
209 600                 605                 610                 615
211 atg gat gcc cac ccc agc cga tac tgt gct act gtg cgg gta cag cga    2106
212 Met Asp Ala His Pro Ser Arg Tyr Cys Ala Thr Val Arg Val Gln Arg
213                 620                 625                 630
215 cca cgg caa gag atc att gaa gac ttg tcc tac atg gtg cgt gag ctc    2154
216 Pro Arg Gln Glu Ile Ile Glu Asp Leu Ser Tyr Met Val Arg Glu Leu
217             635                 640                 645
219 ctc atc caa ttc tac aag tcc acc cgt ttc aag cct acc cgc atc atc    2202
220 Leu Ile Gln Phe Tyr Lys Ser Thr Arg Phe Lys Pro Thr Arg Ile Ile
221         650                 655                 660
223 ttc tac cga gat ggg gtg cct gaa ggc cag cta ccc cag ata ctc cat    2250
224 Phe Tyr Arg Asp Gly Val Pro Glu Gly Gln Leu Pro Gln Ile Leu His
225     665                 670                 675
227 tat gag cta ctg gcc att cgt gat gcc tgc atc aaa ctg gaa aag gac    2298
228 Tyr Glu Leu Leu Ala Ile Arg Asp Ala Cys Ile Lys Leu Glu Lys Asp
229 680                 685                 690                 695
231 tac cag cct ggg atc act tat att gtg gtg cag aaa cgc cat cac acc    2346
232 Tyr Gln Pro Gly Ile Thr Tyr Ile Val Val Gln Lys Arg His His Thr
233                 700                 705                 710
235 cgc ctt ttc tgt gct gac aag aat gag cga att ggg aag agt ggt aac    2394
236 Arg Leu Phe Cys Ala Asp Lys Asn Glu Arg Ile Gly Lys Ser Gly Asn
237             715                 720                 725
239 atc cca gct ggg acc aca gtg gac acc aac atc acc cac cca ttt gag    2442
240 Ile Pro Ala Gly Thr Thr Val Asp Thr Asn Ile Thr His Pro Phe Glu
241         730                 735                 740
243 ttt gac ttc tat ctg tgc agc cac gca ggc atc cag ggc acc agc cga    2490
244 Phe Asp Phe Tyr Leu Cys Ser His Ala Gly Ile Gln Gly Thr Ser Arg
245     745                 750                 755
247 cca tcc cat tac tat gtt ctt tgg gat gac aac cgt ttc aca gca gat    2538
248 Pro Ser His Tyr Tyr Val Leu Trp Asp Asp Asn Arg Phe Thr Ala Asp
249 760                 765                 770                 775
251 gag ctc cag atc ctg acg tac cag ctg tgc cac act tac gta cga tgc    2586
252 Glu Leu Gln Ile Leu Thr Tyr Gln Leu Cys His Thr Tyr Val Arg Cys
253                 780                 785                 790
255 aca cgc tct gtc tct atc cca gca cct gcc tac tat gcc cgc ctg gtg    2634
256 Thr Arg Ser Val Ser Ile Pro Ala Pro Ala Tyr Tyr Ala Arg Leu Val
257             795                 800                 805
259 gct ttc cgg gca cga tac cac ctg gtg gac aag gag cat gac agt gga    2682
260 Ala Phe Arg Ala Arg Tyr His Leu Val Asp Lys Glu His Asp Ser Gly
261         810                 815                 820
263 gag ggg agc cac ata tcg ggg cag agc aat ggg cgg gac ccc cag gcc    2730
264 Glu Gly Ser His Ile Ser Gly Gln Ser Asn Gly Arg Asp Pro Gln Ala
265     825                 830                 835
```

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Input Set : A:\RTS-0236 Sequence Listing.txt
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```
267 ctg gcc aaa gcc gtg cag gtt cac cag gat act ctg cgc acc atg tac    2778
268 Leu Ala Lys Ala Val Gln Val His Gln Asp Thr Leu Arg Thr Met Tyr
269 840                 845                 850                 855
271 ttc gct tga aggcagaacg ctgttacctc actggataga agaaagcttt ccaagcccca 2837
272 Phe Ala
275 ggagctgtgc cacccaaatc cagaggaagc aaggaggagg gaggtggggt agggaggagt  2897
276 gtaggatgcc ttgtttcctt ctatagaggt ggtgtaagag tggggaacag ggccagcaag  2957
277 acagaccacc agccagaaat ctctgatatc aacctcatgt cccccacccc tcaccccatc  3017
278 ttgtcacatc tggccctgac cccactggac caaaaggggc agcactggtg cccaccatac  3077
279 acacaggtgt ctcatgtgac tcacagtgct aaagactcat gcttgacagc ttggtaaggt  3137
280 caactctgta gccctgcaga caaaagctgg ttaggtttgg gtttgatact ttagatggga  3197
281 aagtgagggg cttgagaaag tgggtgggag gagggaagga ttttttagga gccttaatca  3257
282 gaaaaggact agatttgttt aagaagaaaa atgaaaccag acccagatca atattttagg  3317
283 atactagatg ttttaatggg ttcagaatcc agtttgtagg aagatttttt aatggttttg  3377
284 gttgctcctc ccccagctgc cacccccccac cttaccctta ttcctctctg tccacatttt  3437
285 ctgccccacc ttacttctcc tccctgacag acatccagcc cctagtaata cttaaggcac  3497
286 tatggcactt agctttgaag tgacacgacc ctgtcttcct tccgcccgct ggtgggtaac  3557
287 cagtgccttc cctgtaacgg taatgctgca gaactgcaac cttttgtacc tttctttggg  3617
288 gaatggggtg ggggtgggag aggaggtaga tggggaagaa ataccccaga cccaacaaac  3677
289 ctccagccag aaagccagct attttgcatt tgaaggaatt gacttcctca ttcattgagc  3737
290 tttttaaaag atcacaacct caagatggtt aaaatccatt gacatttgca ctttcaaaca  3797
291 tgacaagtct cggagctgct gagatgacag gcccctggcc tttccactta tgcctccttt  3857
292 tctccttatt cctcctacct cccgccccgc ccaggtctgg agttactttc atagcatttt  3917
293 tcactcttgg cttcttttct cccttgatgg tcaagtctct tatgtttcaa tatttcttaa  3977
294 ctggggtgtc ttataacaaa aaactcttag gtctaaaatg agaaaaaaga gagaaaacaa  4037
295 aatgttattt ttataccata acttgagtgt attgccaaaa tttggaaatc cttcccatgc  4097
296 ctgatgagtt tatatcccag aaacattgag ccatcagaat gaactgtgta cctgatttgt  4157
297 tctctgacct ggctaggtag ggaggggggtg gttatcgccc caagatgggg tccaggctcc  4217
298 atccttcctc tgtgcagata ataccttttt cttgctatag cctccctcct ctgcactgtc  4277
299 ctgcactctt tcttgcaagt gcatcttttt ccttcccctg gactgtcctc tgacccttttg  4337
300 gctcatccta gattgcagtg tgtcctgtgg acaggctggg gaattttgct gctccctatt  4397
301 gcttctgttt acaaaaatga atttttcctg gtttcccact agggcatgtg ggtgggtggc  4457
302 atggactttt ttttttttt ttttttgtct tgagacatgg ggtttggctg tcttgcagga  4517
303 ctggagaagg tggtggttct agcttggtct ctgttggcct tgaagcaagc atccccccctg  4577
304 ccctttttcc ttgactgttc attttttttcc tgccccactg cttgggatgg ggagttgcaa  4637
305 cttcagtgtg gaatttcctc tttgaggagc ctgggcttgg atctatcctg atctggtgat  4697
306 gaagccatga ttactttaga cctagcccag gcttggaggc cagctggagg aagaagggtc  4757
307 taaatcctgg cctgtagagt tagaactacc atttcctccc cttagctgcc cttgtatgac  4817
308 ccggatttgc tatgcaaaac aatctatccc aggttctgtt ctggttggct acattgttca  4877
309 gcaactcaca aaacgtagca caaacattca ttatggagaa agcatcagga ctgttgagta  4937
310 actcctcctt tacttttttc ctgctggcta cagcatgggg tgccctatag gcacaagccc  4997
311 agctgaagaa cagaatggag ggctctggga ggaggcagct cactggagag cctacattcc  5057
312 ttacacaagt gcctaaagag agtgatgcta acactccatc tgccctgtcc attgccttca  5117
313 tatacagtct acttcgtgtt ctgtcaccct ttggggaggg gagttctcct gggacagtgg  5177
314 gctctgcatg ttctccactt ggatacattt tggggctagg atcagggcac tattcctgga  5237
315 gggtccagtc attcaccagc atttgcaaat gtccataggg agcaggtggc agcctctact  5297
316 cccagcaaca agtttgtgtt ctctcctttt ctctctttgc ctcactctct ccagttggtt  5357
317 ttcagctggg gcttgaaatg cattttagc cctttgacgt ggcttatgcc attcaagaaa  5417
318 taaaaagcaa gagaatcagc tttgggcaat gacaagaaat gagttcttac tctgattttt  5477
```

Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY DATE: 12/20/2001
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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:825 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:826 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:827 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:939 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:940 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:973 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:974 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:975 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:2246 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
L:2249 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:88
L:2249 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
L:2253 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:88
L:2253 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
L:2254 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:88
L:2254 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4